

ABSTRACT

Disclosed are methods, software, and systems for comparing biopolymer sequences. The model includes at least two different characterizations of states of matching between segments of sequences at defined positions. Examples of states of matching include: similarity and dissimilarity between objects, as well as similarity to a reference, e.g., a reference sequence or a sequence profile. A topology of particular match states can be used to identify classes of sequences, e.g., preprohormone sequences.

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